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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/091,613

DATE: 06/06/2002

TIME: 11:24:27

Input Set : N:\Crf3\RULE60\10091613.raw

Output Set: N:\CRF3\06062002\J091613.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Hillman, Jennifer L.

6 Corley, Neil C.

7 Shah, Purvi

9 (ii) TITLE OF INVENTION: RAS-LIKE PROTEIN

12 (iii) NUMBER OF SEQUENCES: 3

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

16 (B) STREET: 3174 Porter Drive

17 (C) CITY: Palo Alto

18 (D) STATE: CA

19 (E) COUNTRY: USA

20 (F) ZIP: 94304

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Diskette

24 (B) COMPUTER: IBM Compatible

25 (C) OPERATING SYSTEM: DOS

26 (D) SOFTWARE: FastSEQ for Windows Version 2.0

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/10/091,613

C--> 30 (B) FILING DATE: 04-Mar-2002

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/09/198,559

35 (B) FILING DATE:

37 (A) APPLICATION NUMBER: US/08/846,790

38 (B) FILING DATE:

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Billings, Lucy J.

42 (B) REGISTRATION NUMBER: 36,749

43 (C) REFERENCE/DOCKET NUMBER: PF-0388 US

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: 650-855-0555

47 (B) TELEFAX: 650-845-4166

48 (C) TELEX:

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 214 amino acids

55 (B) TYPE: amino acid

56 (C) STRANDEDNESS: single

57 (D) TOPOLOGY: linear

59 (vii) IMMEDIATE SOURCE:

ENTERED

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Input Set : N:\Crf3\RULE60\10091613.raw

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60      (A) LIBRARY: COLNTUT16
61      (B) CLONE: 2791521
62
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64
65      Met Asn Cys Lys Glu Gly Thr Asp Ser Ser Cys Gly Cys Arg Gly Asn
66      1          5          10          15
67      Asp Glu Lys Lys Met Leu Lys Cys Val Val Val Gly Asp Gly Ala Val
68      20          25          30
69      Gly Lys Thr Cys Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu
70      35          40          45
71      Glu Tyr Val Pro Thr Val Phe Asp His Tyr Ala Val Thr Val Thr Val
72      50          55          60
73      Gly Gly Lys Gln His Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu
74      65          70          75          80
75      Asp Tyr Asn Gln Leu Arg Pro Leu Ser Tyr Pro Asn Thr Asp Val Phe
76      85          90          95
77      Leu Ile Cys Phe Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln
78      100         105         110
79      Glu Glu Trp Val Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr
80      115         120         125
81      Val Leu Ile Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu
82      130         135         140
83      Ala Arg Leu Leu Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly
84      145         150         155         160
85      Val Lys Leu Ala Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser
86      165         170         175
87      Ala Leu Thr Gln Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu
88      180         185         190
89      Thr Ile Phe His Pro Lys Lys Lys Lys Arg Cys Ser Glu Gly His
90      195         200         205
91      Ser Cys Cys Ser Ile Ile
92      210
93
94      (2) INFORMATION FOR SEQ ID NO: 2:
95
96      (i) SEQUENCE CHARACTERISTICS:
97
98      (A) LENGTH: 2964 base pairs
99      (B) TYPE: nucleic acid
100     (C) STRANDEDNESS: single
101     (D) TOPOLOGY: linear
102
103     (vii) IMMEDIATE SOURCE:
104
105     (A) LIBRARY: COLNTUT16
106     (B) CLONE: 2791521
107
108     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
109     CCATGTTAGA TGTGACTTGG AAAATGAGAA AGATTTAGCA AAATTCACC GTGTCTTTTG      60
110     CCAGGCTAGA GACAGGGAGA GCAGAGTAAA ACCCTCAGGC TGCTGAAATT TCTAGGCTGT      120
111     TAGGAAGCCC CTCGAATTCT GTGAAAATGA GGGTTTCTTA ACTCACACTG AGAGCGGAAA      180
112     GGGGCAGACC CTTTTCATAA CTCCCTCAAG TGTGTGTTAC CTTTCTTTAC CAGCATGGTA      240
113     AGCAACAGGA CATATCCCAG CCTCGGACAT GTCTGTATGA TCCAAGGTAC CCAAAGTCAG      300
114     ACAGAGTAAA CTCAAGCCTG GCACTGGCTT TCTGCCGCTT CATGTGCTTT GGAAAAAGCA      360
115     GGAGAAGCAA TAGCAGCAGG AGTCCCCAGC AGCTGGAGCC GCAAGAATGA ACTGCAAAGA      420
116     GGGAACTGAC AGCAGCTGCG GCTGCAGGGG CAACGACGAG AAGAAGATGT TGAAGTGTGT      480

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116 GGTGGTGGGG GACGGTGCCG TGGGGAAAAAC CTGCCTGCTG ATGAGCTACG CCAACGACGC 540
117 CTTCCCAGAG GAATACGTGC CCACTGTGTT TGACCACTAT GCAGTTACTG TGA CTGTGGG 600
118 AGGCAAGCAA CACTTGCTCG GACTGTATGA CACCGCGGGA CAGGAGGACT ACAACCAGCT 660
119 GAGGCCACTC TCCTACCCCA ACACGGATGT GTTTTTGATC TGCTTCTCTG TCGTAAACCC 720
120 TGCCTCTTAC CACAATGTCC AGGAGGAATG GGTCCCCGAG CTCAAGGACT GCATGCCTCA 780
121 CGTGCCCTTAT GTCCTCATAG GGACCCAGAT TGATCTCCGT GATGACCCAA AAACCTTGGC 840
122 CCGTTTGCTG TATATGAAAG AGAAACCTCT CACTTACGAG CATGGTGTGA AGCTCGCAA 900
123 AGCGATCGGA GCACAGTGCT ACTTGGAATG TTCAGCTCTG ACTCAGAAAG GTCTCAAAGC 960
124 GGTTTTTGAT GAAGCAATCC TCACCATTTT CCACCCCAAG AAAAAGAAGA AACGCTGTTC 1020
125 TGAGGGTCAC AGCTGCTGTT CAATTATCTG AGGTGTCTG GGACCTGCCT CCACCCATC 1080
126 CAGGGATGAG AATGGCAGCC AATCTCTGTG GCCAAGCTCC AGCCAAAAAG GAGGGCACGA 1140
127 CCAGAAAGGA ACTCCCTTTG CACGGAGGCT TGCCCCATCA CCTCTGAGC CCTCCCAACA 1200
128 CAGCACACTA GTCAGCCAC TGCCACGACC TCCCTGCCAG CCAGAAGCAT CCGTACTGCA 1260
129 CGCTGTCTGA GAATGCTGGG CCTGGATTGC AGACAGTGCC GCTGCTGATC GCATCAAAAA 1320
130 CAAAGTCAAA GGCCATCTCA CATTTTACAA ATCCCCAGCT CATGAACGTG AAGCTGATAG 1380
131 GAAATCACCC CAGGGAACCC GAAAAAGAAA CTTGATTCTT CTATTGCTGG CCTTACTTGA 1440
132 TGTCTTTTAT AAAACTTGGG ACTACAATAC TAACCTTTTT TTCTGAATCT GCTGTTCTAC 1500
133 CCATGTGTCT CACATTCATT TGTATTATTT CAAGAAATGT ACTAATTTCC AGTTCACTCA 1560
134 GGCCTTACTA ATCCATACCA AATTAGCCTA AAGACAAGGC ATTTTATATT CATTTCTATT 1620
135 TTCAGCATGT TTCTACCAAA GCTATTAGAA CCAACACGTA CCTCTGAATG CCCGATTATA 1680
136 AGAAGACATG AGAAGACTTT AAAAGTTTGT GAAATTTACA GAGCCATGAT TTTTGAACCT 1740
137 AATTGAAAGA AAACCATCTG AATTGTTGCA GGTCCACATT TTTGCCAAG ATACACTCTA 1800
138 TAGATGCTTA GTAGTGGCCT GATTTTTTTC CATGTATTGC CACGACAAAC TAAAAATGAA 1860
139 CTGTGTTTAA GAATGTAGTA TTTCTGTTTT TCATCCAAGT TGATTGGGGG AAGAATATGG 1920
140 CAGGATCCAT CTTTTACAGT ATTTTGTATT CAGTAAAGTG GACATTCTCT CTCCTCCCTT 1980
141 CCCCCATTGC ATGCCCTCTT CCTCCCTTGA TTTCACTTTC TCTCATGCCC GGATCCTTTT 2040
142 ATTCTCCCCA GTTATAACCC AGTTATAAAA GAAAGATCTG AGCATAAAGA TACGTGTTTA 2100
143 AAAATAACTA AAAGTAAAGG AAAGTGCCTT AATTTTTCTA TTTGCTTCAA CTGAAAGTGC 2160
144 TTCTCAGCTC GCCCCATGTA AGTTCTCATT CCATGTAAAT GACATTTTCC AGTTACAAC 2220
145 GGTACTGAGA TTTTGCCTCT CTCTTTCCTT ACTCATCCTC CCAAATGTCT TTGTGGGAGC 2280
146 CATATCAGTG GATACCAAGC TCTGTATCCA TTTGTCCCCT GCCCTCCACA ATGTGTGACA 2340
147 TAGAACAGGG ACTTTGGCCC TGGGAAAGCA AAAGCTCCCA GTAAGGAATC CTGTGCCCAA 2400
148 TGATGTAAAA CAATCCAAA CATCCAGGAA TTTTGTATC ATAGAGCGAA TTA CTTCCTA 2460
149 TCTTTTCATT AGAGGCTATG AGGACTTCTA ATTAGTCTTA GTTGCTTATA AGTGCCCTGG 2520
150 AATCACCCAG GTAGGCACTT AATTTTTTTT TCAGTTGCAT GAGCAAAGTG CTTCTTAGTA 2580
151 GTGTGAAATT ACAACAATT TAAGACTTTC CAGATTCAAG CTCCCCTGT TGGAAAAAGC 2640
152 CAGCCTTTCT AATCTCTTCT GCTACTGGAA TAAGCACTTA AGAATTGCGT GATAGCCAGG 2700
153 CACCGTGGCT CATGCCGTGA ATCCCAACAC TTAGGGAGGC TGAGGTGGGT GGGCCGCTTG 2760
154 AGCTCAGGAG TTCAAGACCA GCCTGGGTAA TATAGTGAGA TCCTGTGTCT CTATAAAAAA 2820
155 ATTAAAAATT AGTCAGTTGT AGTGACACAT ACCTGTAGTC CCAGCTACTC AGGAGGCTGA 2880
156 GGTGGAAGGA TCACTTGAGC CCAGAAGGTA AGGCTGCAGT GAGCTGTGAC TGTGCCACTA 2940
157 CACTCCAGCC TGAGTGACAG AGAA 2964

```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

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168          (A) LIBRARY: GenBank
169          (B) CLONE: 190881
171      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
173  Met Pro Gly Ala Gly Arg Ser Ser Met Ala His Gly Pro Gly Ala Leu
174    1          5          10          15
175  Met Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys
176          20          25          30
177  Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro
178    35          40          45
179  Thr Val Phe Asp His Tyr Ala Val Ser Val Thr Val Gly Gly Lys Gln
180    50          55          60
181  Tyr Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg
182    65          70          75          80
183  Leu Arg Pro Leu Ser Tyr Pro Met Thr Asp Val Phe Leu Ile Cys Phe
184          85          90          95
185  Ser Val Val Asn Pro Ala Ser Phe Gln Asn Val Lys Glu Glu Trp Val
186          100          105          110
187  Pro Glu Leu Lys Glu Tyr Ala Pro Asn Val Pro Phe Leu Leu Ile Gly
188    115          120          125
189  Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Asn
190    130          135          140
191  Asp Met Lys Glu Lys Pro Ile Cys Val Glu Gln Gly Gln Lys Leu Ala
192    145          150          155          160
193  Lys Glu Ile Gly Ala Cys Cys Tyr Val Glu Cys Ser Ala Leu Thr Gln
194          165          170          175
195  Lys Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Ile Ala Ile Leu Thr
196          180          185          190
197  Pro Lys Lys His Thr Val Lys Lys Arg Ile Gly Ser Arg Cys Ile Asn
198          195          200          205
199  Cys Cys Leu Ile Thr
200          210

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\06062002\J091613.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]